

ABSTRACT OF THE DISCLOSURE

The invention provides a method for reducing background in hybridization reactions of nucleic acids involving at least two homologous probes, wherein at least one of the probes is nonlinear, or two homologous target sequences and a nonlinear probe. Background is reduced by introducing an intended mismatch with a target sequence in at least one of the probes. The presence of the mismatch reduces the specificity of probes not entirely complementary to a target sequence to such an extent that the background signal is reduced. A set of mixed homologous probes, wherein at least one of the probes is nonlinear, comprising such specific mismatch is also provided. The set can be used for the detection of variants of a family of nucleic acids, for instance, a number of HIV variants. The invention also provides kits for carrying out the methods according to the invention.